

SEQUENCE LISTING

<110> Baxter, John
Fletterick, Robert
Kushner, Peter

<120> NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS

<130> UCAL-246/02/1US

<140> Not Yet Available

<141> 2000-08-10

<150> US 08/980,115

<151> 1997-11-26

<150> US 08/764,870

<151> 1996-12-13

<150> US 60/008,606

<151> 1995-12-14

<150> US 60/008,543

<151> 1995-12-13

<150> US 60/008,540

<151> 1995-12-13

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 410

<212> PRT

<213> Rattus sp.

<220>

<221> DOMAIN

<222> (157)..(410)

<223> minimal ligand binding domain

<220>

<221> DOMAIN

<222> (393)..(405)

<223> activation domain

<400> 1

Met Glu Gln Lys Pro Ser Lys Val Glu Cys Gly Ser Asp Pro Glu Glu
1 5 10 15

Asn Ser Ala Arg Ser Pro Asp Gly Lys Arg Lys Arg Lys Asn Gly Gln
20 25 30

000780-222560

Cys	Pro	Leu	Lys	Ser	Ser	Met	Ser	Gly	Tyr	Ile	Pro	Ser	Tyr	Leu	Asp	35	40	45
Lys	Asp	Glu	Gln	Cys	Val	Val	Cys	Gly	Asp	Lys	Ala	Thr	Gly	Tyr	His	50	55	60
Tyr	Arg	Cys	Ile	Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Thr	65	70	75
Ile	Gln	Lys	Asn	Leu	His	Pro	Thr	Tyr	Ser	Cys	Lys	Tyr	Asp	Ser	Cys	85	90	95
Cys	Val	Ile	Asp	Lys	Ile	Thr	Arg	Asn	Gln	Cys	Gln	Leu	Cys	Arg	Phe	100	105	110
Lys	Lys	Cys	Ile	Ala	Val	Gly	Met	Ala	Met	Asp	Leu	Val	Leu	Asp	Asp	115	120	125
Ser	Lys	Arg	Val	Ala	Lys	Arg	Lys	Leu	Ile	Glu	Gln	Asn	Arg	Glu	Arg	130	135	140
Arg	Arg	Lys	Glu	Glu	Met	Ile	Arg	Ser	Leu	Gln	Gln	Arg	Pro	Glu	Pro	145	150	155
Thr	Pro	Glu	Glu	Trp	Asp	Leu	Ile	His	Val	Ala	Thr	Glu	Ala	His	Arg	165	170	175
Ser	Thr	Asn	Ala	Gln	Gly	Ser	His	Trp	Lys	Gln	Arg	Arg	Lys	Phe	Leu	180	185	190
Pro	Asp	Asp	Ile	Gly	Gln	Ser	Pro	Ile	Val	Ser	Met	Pro	Asp	Gly	Asp	195	200	205
Lys	Val	Asp	Leu	Glu	Ala	Phe	Ser	Glu	Phe	Thr	Lys	Ile	Ile	Thr	Pro	210	215	220
Ala	Ile	Thr	Arg	Val	Val	Asp	Phe	Ala	Lys	Lys	Leu	Pro	Met	Phe	Ser	225	230	235
Glu	Leu	Pro	Cys	Glu	Asp	Gln	Ile	Ile	Leu	Leu	Lys	Gly	Cys	Cys	Met	245	250	255
Glu	Ile	Met	Ser	Leu	Arg	Ala	Ala	Val	Arg	Tyr	Asp	Pro	Glu	Ser	Asp	260	265	270
Thr	Leu	Thr	Leu	Ser	Gly	Glu	Met	Thr	Val	Lys	Arg	Lys	Gln	Leu	Lys	275	280	285
Asn	Gly	Gly	Leu	Gly	Val	Val	Ser	Asp	Ala	Ile	Phe	Glu	Leu	Gly	Lys	290	295	300
Ser	Leu	Ser	Ala	Phe	Asn	Leu	Asp	Asp	Thr	Glu	Val	Ala	Leu	Leu	Gln	305	310	315
Ala	Val	Leu	Leu	Met	Ser	Thr	Asp	Arg	Ser	Gly	Leu	Leu	Cys	Val	Asp	325	330	335

Lys Ile Glu Lys Ser Gln Glu Ala Tyr Leu Leu Ala Phe Glu His Tyr
340 345 350

Val Asn His Arg Lys His Asn Ile Pro His Phe Trp Pro Lys Leu Leu
355 360 365

Met Lys Val Thr Asp Leu Arg Met Ile Gly Ala Cys His Ala Ser Arg
370 375 380

Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Phe Pro Pro Leu
385 390 395 400

Phe Leu Glu Val Phe Glu Asp Gln Glu Val
405 410

<210> 2
<211> 410
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (157)..(410)
<223> minimal ligand binding domain

<400> 2

Met Glu Gln Lys Pro Ser Lys Val Glu Cys Gly Ser Asp Pro Glu Glu
1 5 10 15

Asn Ser Ala Arg Ser Pro Asp Gly Lys Arg Lys Arg Lys Asn Gly Gln
20 25 30

Cys Ser Leu Lys Thr Ser Met Ser Gly Tyr Ile Pro Ser Tyr Leu Asp
35 40 45

Lys Asp Glu Gln Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His
50 55 60

Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr
65 70 75 80

Ile Gln Lys Asn Leu His Pro Thr Tyr Ser Cys Lys Tyr Asp Ser Cys
85 90 95

Cys Val Ile Asp Lys Ile Thr Arg Asn Gln Cys Gln Leu Cys Arg Phe
100 105 110

Lys Lys Cys Ile Ala Val Gly Met Ala Met Asp Leu Val Leu Asp Asp
115 120 125

Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Gln Asn Arg Glu Arg
130 135 140

Arg Arg Lys Glu Glu Met Ile Arg Ser Leu Gln Gln Arg Pro Glu Pro
145 150 155 160

000720 22722900

Thr	Pro	Glu	Glu	Trp	Asp	Leu	Ile	His	Ile	Ala	Thr	Glu	Ala	His	Arg	
				165					170						175	
Ser	Thr	Asn	Ala	Gln	Gly	Ser	His	Trp	Lys	Gln	Arg	Arg	Lys	Phe	Leu	
			180					185					190			
Pro	Asp	Asp	Ile	Gly	Gln	Ser	Pro	Ile	Val	Ser	Met	Pro	Asp	Gly	Asp	
		195					200					205				
Lys	Val	Asp	Leu	Glu	Ala	Phe	Ser	Glu	Phe	Thr	Lys	Ile	Ile	Thr	Pro	
	210					215					220					
Ala	Ile	Thr	Arg	Val	Val	Asp	Phe	Ala	Lys	Lys	Leu	Pro	Met	Phe	Ser	
225					230					235					240	
Glu	Leu	Pro	Cys	Glu	Asp	Gln	Ile	Ile	Leu	Leu	Lys	Gly	Cys	Cys	Met	
				245					250					255		
Glu	Ile	Met	Ser	Leu	Arg	Ala	Ala	Val	Arg	Tyr	Asp	Pro	Glu	Ser	Asp	
			260					265					270			
Thr	Leu	Thr	Leu	Ser	Gly	Glu	Met	Ala	Val	Lys	Arg	Glu	Gln	Leu	Lys	
		275					280						285			
Asn	Gly	Gly	Leu	Gly	Val	Val	Ser	Asp	Ala	Ile	Phe	Glu	Leu	Gly	Lys	
	290					295					300					
Ser	Leu	Ser	Ala	Phe	Asn	Leu	Asp	Asp	Thr	Glu	Val	Ala	Leu	Leu	Gln	
305					310					315					320	
Ala	Val	Leu	Leu	Met	Ser	Thr	Asp	Arg	Ser	Gly	Leu	Leu	Cys	Val	Asp	
				325					330					335		
Lys	Ile	Glu	Lys	Ser	Gln	Glu	Ala	Tyr	Leu	Leu	Ala	Phe	Glu	His	Tyr	
			340					345					350			
Val	Asn	His	Arg	Lys	His	Asn	Ile	Pro	His	Phe	Trp	Pro	Lys	Leu	Leu	
		355					360					365				
Met	Lys	Val	Thr	Asp	Leu	Arg	Met	Ile	Gly	Ala	Cys	His	Ala	Ser	Arg	
	370					375					380					
Phe	Leu	His	Met	Lys	Val	Glu	Cys	Pro	Thr	Glu	Leu	Phe	Pro	Pro	Leu	
385					390					395					400	
Phe	Leu	Glu	Val	Phe	Glu	Asp	Gln	Glu	Val							
				405					410							

```
<210> 3
<211> 461
<212> PRT
<213> Homo sapiens
```

<223> minimal ligand binding domain

<400> 3

Met Thr Pro Asn Ser Met Thr Glu Asn Gly Leu Thr Ala Trp Asp Lys
1 5 10 15
Pro Lys His Cys Pro Asp Arg Glu His Asp Trp Lys Leu Val Gly Met
20 25 30
Ser Glu Ala Cys Leu His Arg Lys Ser His Ser Glu Arg Arg Ser Thr
35 40 45
Leu Lys Asn Glu Gln Ser Ser Pro His Leu Ile Gln Thr Thr Trp Thr
50 55 60
Ser Ser Ile Phe His Leu Asp His Asp Asp Val Asn Asp Gln Ser Val
65 70 75 80
Ser Ser Ala Gln Thr Phe Gln Thr Glu Glu Lys Lys Cys Lys Gly Tyr
85 90 95
Ile Pro Ser Tyr Leu Asp Lys Asp Glu Leu Cys Val Val Cys Gly Asp
100 105 110
Lys Ala Thr Gly Tyr His Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys
115 120 125
Gly Phe Phe Arg Arg Thr Ile Gln Lys Asn Leu His Pro Ser Tyr Ser
130 135 140
Cys Lys Tyr Glu Gly Lys Cys Val Ile Asp Lys Val Thr Arg Asn Gln
145 150 155 160
Cys Gln Glu Cys Arg Phe Lys Lys Cys Ile Tyr Val Gly Met Ala Thr
165 170 175
Asp Leu Val Leu Asp Asp Ser Lys Arg Leu Ala Lys Arg Lys Leu Ile
180 185 190
Glu Glu Asn Arg Glu Lys Arg Arg Arg Glu Glu Leu Gln Lys Ser Ile
195 200 205
Gly His Lys Pro Glu Pro Thr Asp Glu Glu Trp Glu Leu Ile Lys Thr
210 215 220
Val Thr Glu Ala His Val Ala Thr Asn Ala Gln Gly Ser His Trp Lys
225 230 235 240
Gln Lys Pro Lys Phe Leu Pro Glu Asp Ile Gly Gln Ala Pro Ile Val
245 250 255
Asn Ala Pro Glu Gly Gly Lys Val Asp Leu Glu Ala Phe Ser His Phe
260 265 270
Thr Lys Ile Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys

275		280		285
Lys Leu Pro Met Phe Cys Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu				
290		295		300
Leu Lys Gly Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg				
305		310		315 320
Tyr Asp Pro Glu Ser Glu Thr Leu Thr Leu Asn Gly Glu Met Ala Val				
	325		330	335
Ile Arg Gly Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala				
	340		345	350
Ile Phe Asp Leu Gly Met Ser Leu Ser Ser Phe Asn Leu Asp Asp Thr				
	355		360	365
Glu Val Ala Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Pro				
	370		375	380
Gly Leu Ala Cys Val Glu Arg Ile Glu Lys Tyr Gln Asp Ser Phe Leu				
385		390		395 400
Leu Ala Phe Glu His Tyr Ile Asn Tyr Arg Lys His His Val Thr His				
	405		410	415
Phe Trp Pro Lys Leu Leu Met Lys Val Thr Asp Leu Arg Met Ile Gly				
	420		425	430
Ala Cys His Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr				
	435		440	445
Glu Leu Leu Pro Pro Leu Phe Leu Glu Val Phe Glu Asp				
450		455		460

<210> 4
 <211> 416
 <212> PRT
 <213> Homo sapiens

<220>
 <221> DOMAIN
 <222> (131)..(373)
 <223> minimal ligand binding domain

<400> 4

Pro Asn Ser Asn His Val Ala Ser Gly Ala Gly Glu Ala Ala Ile Glu	
1	5 10 15
Thr Gln Ser Ser Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro	
	20 25 30
Pro Pro Leu Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys	
	35 40 45

Ser	Ser	Gly	Tyr	His	Tyr	Gly	Val	Ser	Ala	Cys	Glu	Gly	Cys	Lys	Gly
50						55					60				
Phe	Phe	Arg	Arg	Ser	Ile	Gln	Lys	Asn	Met	Val	Tyr	Thr	Cys	His	Arg
65					70					75					80
Asp	Lys	Asn	Cys	Ile	Ile	Asn	Lys	Val	Thr	Arg	Asn	Arg	Cys	Gln	Tyr
				85					90					95	
Cys	Arg	Leu	Gln	Lys	Cys	Phe	Glu	Val	Gly	Met	Ser	Lys	Glu	Ser	Val
			100				105						110		
Arg	Asn	Asp	Arg	Asn	Lys	Lys	Lys	Lys	Glu	Val	Pro	Lys	Pro	Glu	Cys
		115					120					125			
Ser	Glu	Ser	Tyr	Thr	Leu	Thr	Pro	Glu	Val	Gly	Glu	Leu	Ile	Glu	Lys
	130					135					140				
Val	Arg	Lys	Ala	His	Gln	Glu	Thr	Phe	Pro	Ala	Leu	Cys	Gln	Leu	Gly
145					150					155					160
Lys	Tyr	Thr	Thr	Asn	Asn	Ser	Ser	Glu	Gln	Arg	Val	Ser	Leu	Asp	Ile
				165					170					175	
Asp	Leu	Trp	Asp	Lys	Phe	Ser	Glu	Leu	Ser	Thr	Lys	Cys	Ile	Ile	Lys
			180					185					190		
Thr	Val	Glu	Phe	Ala	Lys	Gln	Leu	Pro	Gly	Phe	Thr	Thr	Leu	Thr	Ile
		195					200					205			
Ala	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Ala	Cys	Leu	Asp	Ile	Leu	Ile
		210				215					220				
Leu	Arg	Ile	Cys	Thr	Arg	Tyr	Thr	Pro	Glu	Gln	Asp	Thr	Met	Thr	Phe
225					230					235					240
Ser	Asp	Gly	Leu	Thr	Leu	Asn	Arg	Thr	Gln	Met	His	Asn	Ala	Gly	Phe
				245					250					255	
Gly	Pro	Leu	Thr	Asp	Leu	Val	Phe	Ala	Phe	Ala	Asn	Gln	Leu	Leu	Pro
			260				265						270		
Leu	Glu	Met	Asp	Asp	Ala	Glu	Thr	Gly	Ile	Leu	Ser	Ala	Ile	Cys	Leu
		275					280					285			
Ile	Cys	Gly	Asp	Arg	Gln	Asp	Leu	Glu	Gln	Pro	Asp	Arg	Val	Asp	Met
		290				295					300				
Leu	Gln	Glu	Pro	Leu	Leu	Glu	Ala	Leu	Lys	Val	Tyr	Val	Arg	Lys	Arg
305					310					315					320
Arg	Pro	Ser	Arg	Pro	His	Met	Phe	Pro	Lys	Met	Leu	Met	Lys	Ile	Thr
				325					330					335	
Asp	Leu	Arg	Ser	Ile	Ser	Ala	Lys	Gly	Ala	Glu	Arg	Val	Ile	Thr	Leu
			340					345					350		


```
<220>
<221> DOMAIN
<222> (231)..(460)
<223> minimal ligand binding domain
```

Met Asp Thr Lys His Phe Leu Pro Leu Asp Phe Ser Thr Gln Val Asn
1 5 10 15

Ser Ser Leu Thr Ser Pro Thr Gly Arg Gly Ser Met Ala Ala Pro Ser
20 25 30

Leu His Pro Ser Leu Gly Pro Gly Ile Gly Ser Pro Gly Gln Leu His
35 40 45

Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn Gly Met Gly Pro Pro
50 55 60

Phe Ser Val Ile Ser Ser Pro Met Gly Pro His Ser Met Ser Val Pro
65 70 75 80

Thr Thr Pro Thr Leu Gly Phe Ser Thr Gly Ser Pro Gln Leu Ser Ser
 85 90 95

Pro Met Asn Pro Val Ser Ser Ser Glu Asp Ile Lys Pro Pro Leu Gly
100 105 110

Leu Asn Gly Val Leu Lys Val Pro Ala His Pro Ser Gly Asn Met Ala
115 120 125

Ser Phe Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly
130 135 140

Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys
145 150 155 160

Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp
165 170 175

Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr
180 185 190

Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu Ala Val Gln Glu Glu
195 200 205

Arg Gln Arg Gly Lys Asp Arg Asn Glu Asn Glu Val Glu Ser Thr Ser
210 215 220

Ser Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu
225 230 235 240

Ala Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu

245	250	255
Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala		
260	265	270
Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His		
275	280	285
Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly		
290	295	300
Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val		
305	310	315
Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser		
325	330	335
Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu		
340	345	350
Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly		
355	360	365
Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser		
370	375	380
Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu		
385	390	395
Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala		
405	410	415
Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys		
420	425	430
Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp		
435	440	445
Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met Thr		
450	455	460

<210> 7
 <211> 525
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> DOMAIN
 <222> (292)..(523)
 <223> minimal ligand binding domain

<400> 7

Met Ser Trp Ala Ala Arg Pro Pro Phe Leu Pro Gln Arg His Ala Glu
1 5 10 15

Gly	Ser	Val	Gly	Arg	Trp	Gly	Ala	Lys	Glu	Cys	Ile	Val	Gly	Ser	Ala	20	25	30
Thr	Ala	Leu	Ala	Gly	Ser	Arg	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Arg	35	40	45
Arg	Arg	Thr	Thr	Asn	Pro	Gly	Ala	Gly	Ala	Arg	Gly	Trp	Thr	Gly	Arg	50	55	60
Asp	Gly	Arg	His	Gly	Arg	Asp	Ser	Arg	Ser	Pro	Asp	Ser	Ser	Ser	Pro	65	70	75
Asn	Pro	Leu	Pro	Gln	Gly	Val	Pro	Pro	Pro	Ser	Pro	Pro	Gly	Pro	Pro	85	90	95
Leu	Pro	Pro	Ser	Thr	Ala	Pro	Thr	Leu	Gly	Gly	Ser	Gly	Ala	Pro	Pro	100	105	110
Pro	Pro	Pro	Met	Pro	Pro	Pro	Pro	Leu	Gly	Ser	Pro	Phe	Pro	Val	Ile	115	120	125
Ser	Ser	Ser	Met	Gly	Ser	Pro	Gly	Leu	Pro	Pro	Pro	Ala	Pro	Pro	Gly	130	135	140
Phe	Ser	Gly	Pro	Val	Ser	Ser	Pro	Gln	Ile	Asn	Ser	Thr	Val	Ser	Leu	145	150	155
Pro	Gly	Gly	Gly	Ser	Gly	Pro	Pro	Glu	Asp	Val	Lys	Pro	Pro	Val	Leu	165	170	175
Gly	Val	Arg	Gly	Leu	His	Cys	Pro	Pro	Pro	Pro	Gly	Gly	Pro	Gly	Ala	180	185	190
Gly	Lys	Arg	Leu	Cys	Ala	Ile	Cys	Gly	Asp	Arg	Ser	Ser	Gly	Lys	His	195	200	205
Tyr	Gly	Val	Tyr	Ser	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Lys	Arg	Thr	210	215	220
Ile	Arg	Lys	Asp	Leu	Thr	Tyr	Ser	Cys	Arg	Asp	Asn	Lys	Asp	Cys	Thr	225	230	235
Val	Asp	Lys	Arg	Gln	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	Arg	Tyr	Gln	Lys	245	250	255
Cys	Leu	Ala	Thr	Gly	Met	Lys	Arg	Glu	Ala	Val	Gln	Glu	Glu	Arg	Gln	260	265	270
Arg	Gly	Lys	Asp	Lys	Asp	Gly	Asp	Gly	Glu	Cys	Ala	Gly	Gly	Ala	Pro	275	280	285
Glu	Glu	Met	Pro	Val	Asp	Arg	Ile	Leu	Glu	Ala	Glu	Leu	Ala	Val	Glu	290	295	300
Gln	Lys	Ser	Asp	Gln	Gly	Val	Glu	Gly	Pro	Gly	Gly	Thr	Gly	Gly	Ser	305	310	315

85								90								95													
Phe	Phe	Arg	Arg	Thr	Ile	Arg	Met	Lys	Leu	Glu	Tyr	Glu	Lys	Cys	Glu														
			100					105						110															
Arg	Ser	Cys	Lys	Ile	Gln	Lys	Lys	Asn	Arg	Asn	Lys	Cys	Gln	Tyr	Cys														
		115					120					125																	
Arg	Phe	Gln	Lys	Cys	Leu	Ala	Leu	Gly	Met	Ser	His	Asn	Ala	Ile	Arg														
	130					135					140																		
Phe	Gly	Arg	Met	Pro	Glu	Ala	Glu	Lys	Arg	Lys	Leu	Val	Ala	Gly	Leu														
145					150					155					160														
Thr	Ala	Asn	Glu	Gly	Ser	Gln	Tyr	Asn	Pro	Gln	Val	Ala	Asp	Leu	Lys														
				165					170					175															
Ala	Phe	Ser	Lys	His	Ile	Tyr	Asn	Ala	Tyr	Leu	Lys	Asn	Phe	Asn	Met														
			180					185					190																
Thr	Lys	Lys	Lys	Ala	Arg	Ser	Ile	Leu	Thr	Gly	Lys	Ala	Ser	His	Thr														
		195					200					205																	
Ala	Pro	Phe	Val	Ile	His	Asp	Ile	Glu	Thr	Leu	Trp	Gln	Ala	Glu	Lys														
	210					215					220																		
Gly	Leu	Val	Trp	Lys	Gln	Leu	Val	Asn	Gly	Leu	Pro	Pro	Tyr	Lys	Glu														
225					230					235					240														
Ile	Ser	Val	His	Val	Phe	Tyr	Arg	Cys	Gln	Cys	Thr	Thr	Val	Glu	Thr														
			245						250					255															
Val	Arg	Glu	Leu	Thr	Glu	Phe	Ala	Lys	Ser	Ile	Pro	Ser	Phe	Ser	Ser														
			260					265					270																
Leu	Phe	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	His	Glu														
	275						280					285																	
Ala	Ile	Phe	Ala	Met	Leu	Ala	Ser	Ile	Val	Asn	Lys	Asp	Gly	Leu	Leu														
	290					295					300																		
Val	Ala	Asn	Gly	Ser	Gly	Phe	Val	Thr	Arg	Glu	Phe	Leu	Arg	Ser	Leu														

385 390 395 400

Gln Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met
405 410 415

Met Gln Arg Ile Lys Lys Thr Glu Thr Glu Thr Ser Leu His Pro Leu
420 425 430

Leu Gln Glu Ile Tyr Lys Asp Met Tyr
435 440

<210> 10

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (202)..(475)

<223> minimal ligand binding domain

<400> 10

Met Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser
1 5 10 15

Ser Val Asp Leu Ser Met Met Asp Asp His Ser His Ser Phe Asp Ile
20 25 30

Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Ala Pro His Tyr
35 40 45

Glu Asp Ile Pro Phe Thr Arg Ala Asp Pro Met Val Ala Asp Tyr Lys
50 55 60

Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro
65 70 75 80

Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Ala Gln Leu Tyr Asn Arg Pro
85 90 95

His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys
100 105 110

Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly
115 120 125

Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp
130 135 140

Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys
145 150 155 160

Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
165 170 175

Ala	Ile	Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	
			180													185
Ala	Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp	
		195					200					205				
Leu	Arg	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe	
	210					215					220					
Pro	Leu	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr	
225					230					235					240	
Asp	Lys	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly	
				245					250					255		
Glu	Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser	
			260					265					270			
Lys	Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	
	275						280					285				
Glu	Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Asn	Ile	Pro	Gly	Phe	
	290					295					300					
Ile	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	
305					310					315					320	
His	Glu	Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly	
			325						330					335		
Val	Leu	Ile	Ser	Glu	Gly	Gln	Gly	Phe	Met	Thr	Arg	Glu	Phe	Leu	Lys	
			340					345					350			
Ser	Leu	Arg	Lys	Pro	Phe	Gly	Asp	Phe	Met	Glu	Pro	Lys	Phe	Glu	Phe	
		355					360					365				
Ala	Val	Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Leu	Ala	Ile	
	370					375					380					
Phe	Ile	Ala	Val	Ile	Ile	Leu	Ser	Gly	Asp	Arg	Pro	Gly	Leu	Leu	Asn	
385					390					395					400	
Val	Lys	Pro	Ile	Glu	Asp	Ile	Gln	Asp	Asn	Leu	Leu	Gln	Ala	Leu	Glu	
			405						410					415		
Leu	Gln	Leu	Lys	Leu	Asn	His	Pro	Glu	Ser	Ser	Gln	Leu	Phe	Ala	Lys	
			420					425					430			
Val	Leu	Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	Glu	His	Val	
	435						440					445				
Gln	Leu	Leu	His	Val	Ile	Lys	Lys	Thr	Glu	Thr	Asp	Met	Ser	Leu	His	
	450					455					460					
Pro	Leu	Leu	Gln	Glu	Ile	Tyr	Lys	Asp	Leu	Tyr						
465					470					475						

[illegible]

<400> 11

Glu Gln Leu Leu Gly Ser Cys Thr Leu Lys Phe Pro Ala Gln Asp Ala
20 25 30

Gln Val Ile Val Met Ser Gly Gln Glu Thr Ile Arg Val Leu Glu Val
35 40 45

Glu Val Asp Thr Ala Leu Ser Ser Ala Gly Ala Ala Glu Ser Gly Gly
50 55 60

Asp Glu Glu Gly Ser Gly Gln Ser Leu Glu Ala Thr Glu Glu Ala Gln
65 70 75 80

Leu Asp Gly Pro Val Thr Thr Ser Ser Thr Thr Ala Val Thr Val Glu
85 90 95

Val Ser Ala Pro Val Val Gln Thr Val Val Ser Lys Ala Ala Ile Ser
100 105 110

Val Ser Pro Ala Gln Gln Thr Ser Val Pro Ile Thr Val Gln Ala Cys
115 120 125

Pro Gln Val Leu Thr Gln Asp Gly Leu Ala Ser Leu Met Thr Gly Met
130 135 140

Leu Ala Gln Gln Ser Ser Leu Gly Gln Pro Leu Leu Ile Pro Leu Ser
145 150 155 160

Met Ala Gly Ser Val Gly Gly Gln Gly Gly Leu Ala Val Leu Thr Leu
165 170 175

Pro Thr Ala Thr Val Ala Thr Leu Pro Gly Leu Ala Ala Ala Ser Pro
180 185 190

Ala Gly Gly Leu Leu Lys Leu Pro Phe Ala Gly Leu Gln Ala Ala Thr
195 200 205

Val Leu Asn Ser Val Gln Thr Gln Leu Gln Ala Pro Ala Gln Ala Val
210 215 220

Leu Gln Pro Gln Met Ser Ala Leu Ala Met Gln Gln Thr Gln Thr Thr
225 230 235 240

Ala Ala Thr Thr Ala Ser Ile Val Gln Lys Ala Ser Glu Pro Ser Val
245 250 255

Ser Val Ala Thr Leu Gln Thr Ala Gly Leu Ser Ile Asn Pro Ala Ile
260 265 270

Ile Ser Ala Ala Ser Leu Gly Ala Gln Pro Gln Phe Ile Ser Ser Leu
275 280 285

Thr Thr Thr Pro Ile Ile Thr Ser Ala Met Ser Asn Val Ala Gly Leu
290 295 300

Thr Ser Gln Leu Ile Thr Asn Ala Gln Gly Gln Val Ile Gly Thr Leu
305 310 315 320

Pro Leu Leu Val Asn Pro Ala Ser Leu Ala Gly Ala Ala Ala Ala Ser
325 330 335

Ala Leu Pro Ala Gln Gly Leu Gln Val Gln Thr Val Ala Pro Gln Leu
340 345 350

Leu Leu Asn Ser Gln Gly Gln Ile Ile Ala Thr Ile Gly Asn Gly Pro
355 360 365

Thr Ala Ala Ile Pro Ser Thr Ala Ser Val Leu Pro Lys Ala Thr Val
370 375 380

Pro Leu Thr Leu Thr Lys Thr Thr Thr Gln Gly Pro Val Gly Lys Val
385 390 395 400

Ala Pro Ser Lys Val Ile Ile Ala Pro Gln Pro Ser Val Val Lys Pro
405 410 415

Val Thr Ser Leu Thr Ala Ala Gly Val Ile Ala Cys Gly Glu Met Pro
420 425 430

Thr Val Gly Gln Leu Val Asn Lys Pro Ser Ala Val Lys Asp Glu Glu
435 440 445

Ala Ile Asn Leu Glu Glu Ile Arg Glu Phe Ala Lys Asn Phe Lys Ile
450 455 460

Arg Arg Leu Ser Leu Gly Leu Thr Gln Thr Gln Val Gly Gln Ala Leu
465 470 475 480

Thr Ala Thr Glu Gly Pro Ala Tyr Ser Gln Ser Ala Ile Cys Arg Phe
485 490 495

Glu Lys Leu Asp Ile Thr Pro Lys Ser Ala Gln Lys Leu Lys Pro Val
500 505 510

Leu Glu Arg Trp Leu Ala Glu Ala Glu Leu Trp Asn Gln Lys Gly Gln
515 520 525

Gln Asn Leu Met Glu Phe Val Gly Gly Glu Pro Ser Lys Lys Arg Lys
530 535 540

145		150		155		160
Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met						
		165		170		175
Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala						
		180		185		190
Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe						
		195		200		205
Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr						
		210		215		220
Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys						
		225		230		235
Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg						
		245		250		255
Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp						
		260		265		270
Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala						
		275		280		285
Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn						
		290		295		300
Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu						
		305		310		315
Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro						
		325		330		335
Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg						
		340		345		350
Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val						
		355		360		365
Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu						
		370		375		380
Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly						
		385		390		395
Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys						
		405		410		415
Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser						
		420		425		430
Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu						
		435		440		445
Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser						

000730-2212360

450

455

460

Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
465 470 475 480

Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
485 490 495

Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
500 505 510

His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
515 520 525

Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
530 535 540

Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
545 550 555 560

Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
565 570 575

His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
580 585 590

Ala Thr Val
595

<210> 13
<211> 777
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (506)..(762)
<223> minimal ligand binding domain

<400> 13

Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
1 5 10 15

Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
20 25 30

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
35 40 45

Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50 55 60

Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65 70 75 80

000180 22722960

0000130-2272560

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
85 90 95

Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100 105 110

Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
115 120 125

Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
130 135 140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
145 150 155 160

Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
165 170 175

Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
180 185 190

Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
195 200 205

Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
210 215 220

Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
225 230 235 240

Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
245 250 255

Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
260 265 270

Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
275 280 285

Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
290 295 300

Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
305 310 315 320

Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
325 330 335

Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn
340 345 350

Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
355 360 365

Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
370 375 380

Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
 385 390 395 400
 Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro
 405 410 415
 Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
 420 425 430
 Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
 435 440 445
 Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile
 450 455 460
 Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys
 465 470 475 480
 Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys Lys
 485 490 495
 Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly Val Ser Gln Glu Thr Ser
 500 505 510
 Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu
 515 520 525
 Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu
 530 535 540
 Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Thr Trp Arg Ile Met
 545 550 555 560
 Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala Ala Val Lys
 565 570 575
 Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln
 580 585 590
 Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala Phe Ala Leu
 595 600 605
 Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala
 610 615 620
 Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr
 625 630 635 640
 Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu
 645 650 655
 Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu Leu
 660 665 670
 Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu
 675 680 685

Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg
690 695 700

Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys
705 710 715 720

Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys
725 730 735

Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met
740 745 750

Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn
755 760 765

Ile Lys Lys Leu Leu Phe His Gln Lys
770 775

<210> 14
<211> 933
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (659)..(918)
<223> minimal ligand binding domain

<400> 14

Met Thr Glu Leu Lys Ala Lys Gly Pro Arg Ala Pro His Val Ala Gly
1 5 10 15

Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
20 25 30

Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

0066743-081000

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
 450 455 460
 Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
 465 470 475 480
 Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
 485 490 495
 Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
 500 505 510
 Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
 515 520 525
 Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
 530 535 540
 Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
 545 550 555 560
 Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
 565 570 575
 Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
 580 585 590
 Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
 595 600 605
 Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
 610 615 620
 Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys
 625 630 635 640
 Lys Phe Asn Lys Val Arg Val Val Arg Ala Leu Asp Ala Val Ala Leu
 645 650 655
 Pro Gln Pro Leu Gly Val Pro Asn Glu Ser Gln Ala Leu Ser Gln Arg
 660 665 670
 Phe Thr Phe Ser Pro Gly Gln Asp Ile Gln Leu Ile Pro Pro Leu Ile
 675 680 685
 Asn Leu Leu Met Ser Ile Glu Pro Asp Val Ile Tyr Ala Gly His Asp
 690 695 700
 Asn Thr Lys Pro Asp Thr Ser Ser Ser Leu Leu Thr Ser Leu Asn Gln
 705 710 715 720
 Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu
 725 730 735
 Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln
 740 745 750

000780 2272550

45

Val Asn Asn Ala Phe Ser Tyr Thr Ala Ser Gly Thr Ser Ala Gly Ser

340								345				350							
Ser	Thr	Leu	Arg	Asp	Val	Val	Pro	Ser	Pro	Asp	Thr	Gln	Glu	Lys	Gly				
		355					360					365							
Ala	Gln	Glu	Val	Pro	Phe	Pro	Lys	Thr	Glu	Glu	Val	Glu	Ser	Ala	Ile				
	370					375					380								
Ser	Asn	Gly	Val	Thr	Gly	Gln	Leu	Asn	Ile	Val	Gln	Tyr	Ile	Lys	Pro				
385					390					395					400				
Glu	Pro	Asp	Gly	Ala	Phe	Ser	Ser	Ser	Cys	Leu	Gly	Gly	Asn	Ser	Lys				
				405					410					415					
Ile	Asn	Ser	Asp	Ser	Ser	Phe	Ser	Val	Pro	Ile	Lys	Gln	Glu	Ser	Thr				
			420						425				430						
Lys	His	Ser	Cys	Ser	Gly	Thr	Ser	Phe	Lys	Gly	Asn	Pro	Thr	Val	Asn				
		435					440					445							
Pro	Phe	Pro	Phe	Met	Asp	Gly	Ser	Tyr	Phe	Ser	Phe	Met	Asp	Asp	Lys				
	450					455					460								
Asp	Tyr	Tyr	Ser	Leu	Ser	Gly	Ile	Leu	Gly	Pro	Pro	Val	Pro	Gly	Phe				
465					470					475					480				
Asp	Gly	Asn	Cys	Glu	Gly	Ser	Gly	Phe	Pro	Val	Gly	Ile	Lys	Gln	Glu				
				485					490					495					
Pro	Asp	Asp	Gly	Ser	Tyr	Tyr	Pro	Glu	Ala	Ser	Ile	Pro	Ser	Ser	Ala				
			500					505					510						
Ile	Val	Gly	Val	Asn	Ser	Gly	Gly	Gln	Ser	Phe	His	Tyr	Arg	Ile	Gly				
		515					520					525							
Ala	Gln	Gly	Thr	Ile	Ser	Leu	Ser	Arg	Ser	Ala	Arg	Asp	Gln	Ser	Phe				
	530					535					540								
Gln	His	Leu	Ser	Ser	Phe	Pro	Pro	Val	Asn	Thr	Leu	Val	Glu	Ser	Trp				
545					550					555					560				
Lys	Ser	His	Gly	Asp	Leu	Ser	Ser	Arg	Arg	Ser	Asp	Gly	Tyr	Pro	Val				
				565					570					575					
Leu	Glu	Tyr	Ile	Pro	Glu	Asn	Val	Ser	Ser	Ser	Thr	Leu	Arg	Ser	Val				
			580					585					590						
Ser	Thr	Gly	Ser	Ser	Arg	Pro	Ser	Lys	Ile	Cys	Leu	Val	Cys	Gly	Asp				
		595					600					605							
Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Val	Val	Thr	Cys	Gly	Ser	Cys	Lys				
	610					615					620								
Val	Phe	Phe	Lys	Arg	Ala	Val	Glu	Gly	Gln	His	Asn	Tyr	Leu	Cys	Ala				
625					630					635					640				
Gly	Arg	Asn	Asp	Cys	Ile	Ile	Asp	Lys	Ile	Arg	Arg	Lys	Asn	Cys	Pro				

000750-2272960

645	650	655
Ala Cys Arg Leu Gln Lys Cys Leu Gln Ala Gly Met Asn Leu Gly Ala 660	665	670
Arg Lys Ser Lys Lys Leu Gly Lys Leu Lys Gly Ile His Glu Glu Gln 675	680	685
Pro Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro Gln Ser Pro 690	695	700
Glu Glu Gly Thr Thr Tyr Ile Ala Pro Ala Lys Glu Pro Ser Val Asn 705	710	715
Thr Ala Leu Val Pro Gln Leu Ser Thr Ile Ser Arg Ala Leu Thr Pro 725	730	735
Ser Pro Val Met Val Leu Glu Asn Ile Glu Pro Glu Ile Val Tyr Ala 740	745	750
Gly Tyr Asp Ser Ser Lys Pro Asp Thr Ala Glu Asn Leu Leu Ser Thr 755	760	765
Leu Asn Arg Leu Ala Gly Lys Gln Met Ile Gln Val Val Lys Trp Ala 770	775	780
Lys Val Leu Pro Gly Phe Lys Asn Leu Pro Leu Glu Asp Gln Ile Thr 785	790	795
Leu Ile Gln Tyr Ser Trp Met Cys Leu Ser Ser Phe Ala Leu Ser Trp 805	810	815
Arg Ser Tyr Lys His Thr Asn Ser Gln Phe Leu Tyr Phe Ala Pro Asp 820	825	830
Leu Val Phe Asn Glu Glu Lys Met His Gln Ser Ala Met Tyr Glu Leu 835	840	845
Cys Gln Gly Met His Gln Ile Ser Leu Gln Phe Val Arg Leu Gln Leu 850	855	860
Thr Phe Glu Glu Tyr Thr Ile Met Lys Val Leu Leu Leu Leu Ser Thr 865	870	875
Ile Pro Lys Asp Gly Leu Lys Ser Gln Ala Ala Phe Glu Glu Met Arg 885	890	895
Thr Asn Tyr Ile Lys Glu Leu Arg Lys Met Val Thr Lys Cys Pro Asn 900	905	910
Asn Ser Gly Gln Ser Trp Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu 915	920	925
Asp Ser Met His Asp Leu Val Ser Asp Leu Leu Glu Phe Cys Phe Tyr 930	935	940
Thr Phe Arg Glu Ser His Ala Leu Lys Val Glu Phe Pro Ala Met Leu		

960

975

980

<213> Homo sapiens

<223> minimal ligand binding domain

<400>

15

30

45

60

80

95

110

125

140

160

175

190

Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn
 195 200 205
 Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn
 210 215 220
 Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu
 225 230 235 240
 Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro
 245 250 255
 Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr
 260 265 270
 Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr
 275 280 285
 Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn
 290 295 300
 Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met
 305 310 315 320
 Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu
 325 330 335
 Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp
 340 345 350
 Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile
 355 360 365
 Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser
 370 375 380
 Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln
 385 390 395 400
 Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys
 405 410 415
 Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile
 420 425 430
 Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr
 435 440 445
 Phe His Thr Gln
 450

<210> 17
 <211> 16
 <212> DNA
 <213> Artificial/Unknown
 <220>

